Sequence Length: 40

SEQUENCE LISTING

Obgodica Biolino	
SEQ ID NO: 1	
Sequence Length: 40	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG	40
SEQ ID NO: 2	
Sequence Length: 39	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT	39
SEQ ID NO: 3	
Sequence Length: 40	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSGTTG	40
SEQ ID NO: 4	
Sequence Length: 43	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG	43
SEQ ID NO: 5	

Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGGATTTWC AGGTGCAGAT TWTCAGCTTC 40 SEO ID NO: 6 Sequence Length: 37 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGAGGTKCY YTGYTSAGYT YCTGRGG 37 SEQ ID NO: 7 Sequence Length: 41 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G 41 SEQ ID NO: 8 Sequence Length: 41 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGTGGGGAY CTKTTTYCMM TTTTTCAATT G 41 SEO ID NO: 9 Sequence Length: 35 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear

At A control of the many and a transfer of the many	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGTRTCCW CASCTCAGTT CCTTG	35
SEQ ID NO: 10	
Sequence Length: 37	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTTCT	37
SEQ ID NO: 11	
Sequence Length: 38	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGAAGCCC CAGCTCAGCT TCTCTTCC	38
SEQ ID NO: 12	
Sequence Length: 27	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGATCCCGGG TGGATGGTGG GAAGATG	27
SEQ ID NO: 13	
Sequence Length: 37	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGAAATGCA GCTGGGTCAT STTCTTC	37

SEQ ID NO: 14	
Sequence Length: 36	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topclogy: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT	36
SEQ ID NO: 15	
Sequence Length: 37	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGAAGWTGT GGTTAAACTG GGTTTTT	37
SEQ ID NO: 16	
Sequence Length: 35	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGRACTTTG GGYTCAGCTT GRTTT	35
SEQ ID NO: 17	
Sequence Length: 40	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGACTCCA GGCTCAATTT AGTTTTCCTT	40
SEQ ID NO: 18	
Sequence Length: 37	
Sequence Type: Nucleic acid	

Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC 37 SEO ID NO: 19 Sequence Length: 36 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT 36 SEQ ID NO: 20 Sequence Length: 33 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGAGAGTGC TGATTCTTTT GTG 33 SEQ ID NO: 21 Sequence Length: 40 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCTG 40 SEQ ID NO: 22 Sequence Length: 37 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear

Molecular Type: Synthetic DNA

Sequence	
ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCTG	37
SEQ ID NO: 23	
Sequence Length: 38	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGATTTTG GGCTGATTTT TTTTATTG	38
SEQ ID NO: 24	
Sequence Length: 37	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGATGGTGT TAAGTCTTCT GTACCTG	37
SEQ ID NO: 25	
Sequence Length: 28	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGATCCCGGG CCAGTGGATA GACAGATG	28
SEQ ID NO: 26	
Sequence Length: 382	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: cDNA	
Original Source	
Organism: Mouse	
Immediate Source	

Clone: pUC-M21-V, Features: 1..72 sig peptide 73..382 mat peptide Sequence 48 ATG GAG TCA CAT ATT CAG GTC TTT GTA TAC ATG TTG CTG TGG TTG TCT Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser 10 15 5 GGT GTT GAT GGA GAC ATT GTG ATG ACC CAG TCT CAA AAA TTC ATG TCC 96 Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser 25 20 ACA TCA GTA GGA GAC AGG GTC AGC GTC ACC TGC AAG GCC AGT GAG AAT 144 Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn 35 GTG GGT ACT AAT GTA GCC TGG TAT CAA CAG AAA CCA GGG CAA TCT CCT 192 Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro 50 55 240 AAA CCA CTG ATT TAC TCG GCA TCC TAT CGG TAC AGT GGA GTC CCT GAT Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp 75 65 70 CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC ACC 288 Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr 90 85 AAT GTG CAG TCT GAA GAC TTG GCA GAC TAT TTC TGT CAG CAA TAT AAC 336 Awn Val Gin Ser Giu Asp Leu Ala Asp Tyr Phe Cys Gin Gin Tyr Asn 100 105 AGC TAT CCT CGG GCG TTC GGT GGA GGC ACC AAA CTG GAA ATC AAA C 382 Ser Tyr Pro Arg Ala Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys 115 120 125 SEO ID NO: 27 Sequence Length: 409 Sequence Type: Nucleic acid

Strandedness: Double Topology: Linear

Molecular Type: cDNA Original Source Organism: Mouse Immediate Source Clone: pUC-M21-Vn Features: 1..57 sig peptide 58..409 mat peptide Sequence ATG AAA TGC AGC TGG GTC ATG TTC TTC CTG ATG GCA CTG GTT ACA GGG 48 Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly 10 GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG 96 Val Asn Ser Glu Val Gln Lau Gln Gln Ser Gly Ala Glu Leu Val Lys 20 25 CCA GGG GCC TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT 144 Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile 35 40 AAA GAC ACC TAT ATA CAC TGG GCG AAG CAG AGG CCT GAA CAG GGC CTG 192 Lys Asp Thr Tyr Ile His Trp Ale Lys Gln Arg Pro Glu Gln Gly Leu 50 55 GAG TGG ATT GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC 240 Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp 20 CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC 288 Pro Lys Phe Gin Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn 85 90 95 ACA GCC TAC CTG CAG CTC AGC GTG ACA TCT GAG GAC ACT GCC GTC 336 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val 100 105 110 TAT TAC TGT GCT TCG GCC TAC TAT GTT AAC CAG GAC TAC TGG GGT CAA 384

Tyr Tyr Cys Ala Ser Ala Tyr Tyr Vai Asn Gln Asp Tyr Trp Gly Gln

125

120

115

. .

GGA ACC TCA GTC ACC GTC TCC TCA G	409
Gly Thr Ser Val Thr Val Ser Ser	409
130 135	
SEO ID NO: 28	
Sequence Length: 34	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence GATAAGCTTC CACCATGGGC TTCAAGATGG AGTC	34
	34
SEQ ID NO: 29	
Sequence Length: 34	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGCGGATCCA CTCACGTTTG ATTTCCAGTT TGGT	34
SEQ ID NO: 30	
Sequence Length: 43	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GATAAGCTTC CACCATGAAA TGCAGCTGGG TCATGTTCTT CCT	43
SEQ ID NO: 31	
Sequence Length: 34	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGCGGATCCA CTCACCTGAG GAGACGGTGA CTGA	34

SEQ ID NO: 32 Sequence Length: 18 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence CAGACAGTGG TTCAAAGT 18 SEO ID NO: 33 Sequence Length: 26 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GAATTCGGAT CCACTCACGT TTGATT 26 SEQ ID NO: 34 Sequence Length: 44 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC 44 SEO ID NO: 35 Sequence Length: 38 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence TCCTATCGGT ACAGTGGTGT GCCAAGCAGA TTCAGCGG 38 SEQ ID NO: 36 Sequence Length: 47

Sequence Type: Nucleic acid

. . - • Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG 47 SEO ID NO: 37 Sequence Length: 44 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 44 ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC SEQ ID NO: 38 Sequence Length: 47 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG 47 SEQ ID NO: 39 Sequence Length: 44 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GGATAGCTGT TATATTGCTG GCAGTAGTAG GTAGCGATGT CCTC 44 SEO ID NO: 40 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear

Molecular Type: Synthetic

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Ori	gina	al S	our	ce												
	0:	cgar	ıism	: 1	Mous	e a	nd :	huma	n							
Imm	edia	ate	Sou	rce												
	C.	lone	:	HEF	-RVI	-M2	la-	gĸ								
	Ar	ninc	ac	id ·	-19-	-1:	lea	der								
	Aı	ninc	ac	id	1	- 2	3 : F	Ri								
	Aı	nino	ac	id	24	- 3	4 : C	DR1								
	Aı	nino	ac	id	35	- 4	9:F	R2								
	Aı	ninc	ac	id	50	- 5	6 : C	DR2								
	A	mino	ac	id	57	- 8	8 : F	R3								
	Aı	mino	ac	id	89	- 9	7 : C	DR3								
	A	mino	ac	id	98	- 1	07:	FR4								
Seq	uen	ce														
ATG	GGA	TGG	ACC	TGT	ATC	ATC	CTC	TCC	TTG	GTA	GCA	ACA	CCT	ACA	GGT	48
Met	GLy	Trp	Ser	Cys	Ile	Ile	Leu	Ser		Val	Ala	Thr	Ala		Gly	
-19				15					-10					-5		
crc.	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	ACC	AGC	CTG	AGC	GCC	96
								Gln								,-
		-1	1					5					10			
															GTG	144
Ser	Val	Gly 15		Arg	Val	Thr	20	Thr	Cys	Lys	VTE	ser 25	GIT	Asn	ASI	
		13					20					2.5				
GGT	ACT	AAT	GTA	GCC	TGG	TAC	ÇAG	CAG	AAG	CCA	GGA	AAG	GCT	CCA	AAG	192
Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
	30					35					40					
crc	CTG	ATC	TAC	TCG	GC A	TCC	TAT	cee	TAC	AGT	CCT	GTG	CCA	≜ GC	AGA	240
															Arg	
45		-	•		50		•	Ū	•	55					60	
TTC	AGC	CCT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	288

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

70

75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Fro Giu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGC ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gin Gly Thr Lys Val Glu Ile Lys	
95 100 105	
SEQ ID NO: 41	
Sequence Length: 31	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGTACCGACT ACACCTTCAC CATCAGCAGC C	31
SEQ ID NO: 42	
Sequence Length: 31	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGTGAAGGTG TAGTCGGTAC CGCTACCGCT A	31
SEQ ID NO: 43	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	
Immediate Source	
Clone: HEF-RVL-M21b-gk	
Amino acid -191:leader	
Amino acid 1 - 23:FR1	
Amino acid 24 - 34:CDR1	

Amino acid	35 - 49:FR2		
Amino acid	50 - 56:CDR2		
Amino acid	57 - 88:FR3		
Amino acid	89 - 97:CDR3		
Amino acid	98 - 107:FR4		
Sequence			
ATG GGA TGG AGC TGT	ATC ATC CTC TCC	TTG GTA GCA ACA	GCT ACA GGT 48
Met Gly Trp Ser Cys			
-19 -15		-10	-5
GTC CAC TCC GAC ATC			
Val His Ser Asp Ile	Gin Met Thr Gin 3	Ser Pro Ser Ser I	len ser ala 10
-1 1	,		**
AGC GTG GGT GAC AGA	GTG ACC ATC ACC	TGT AAG GCC AGT	CAG AAT GTG 144
Ser Val Gly Asp Arg	Val Thr Ile Thr	Cys Lys Ala Ser	31n Asn Val
15	20	25	
GGT ACT AAT GTA GCC			
Gly Thr Asn Val Ala	35	Lys Pro Gly Lys A	NIE PEO LYS
30	33		
CTG CTG ATC TAC TCG	GCA TCC TAT CGG	TAC AGT GGT GTG	CCA AGC AGA 240
Leu Leu Ile Tyr Ser	Ala Ser Tyr Arg	Tyr Ser Gly Val	Pro Ser Arg .
45	50	55	60
		MAG AGG MMG AGG	ATC AGC AGC 288
TTC AGC GGT AGC GGT Phe Ser Gly Ser Gly			
fine ser dry ser dry	ser dry lift asp	70	75
CTC CAG CCA GAG GAC	ATG GCC ACC TAC	TAC TGC CAG CAA	TAT AAC AGC 336
Leu Gln Pro Glu Asp	Ile Ala Thr Tyr	Tyr Cys Gln Gln	Tyr Asn Ser
80 .	85		90
TAT CCT CGG GCG TTC	GEO CAA GGG ACC	AAG GTG GAA ATC	AAA C 379
Tyr Pro Arg Ala Phe			
95	100	105	•
SEQ ID NO: 44			
Sequence Length:	29		
Sequence Type:	Nucleic acid		

Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 29 GCTACCTACT TCTGCCAGCA ATATAACAG SEQ ID NO: 45 Sequence Length: 29 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 29 TGCTGGCAGA AGTAGGTAGC GATGTCCTC SEQ ID NO: 46 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21c-gx Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4 Sequence 48 ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -10 -5 -15

GTC	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	96
val	His	Ser	Asp	Ile	Gln	Me t	Thr	G1n	Ser	Pro	Ser	Ser	Leu	Ser	Ala	
		-1	1					5					10			
					GTG		150		TOT		000	400	CAG	447	OTO	144
					Va1											144
361	141	15	woh	n. F	***		20		0,5	2,3		2.5	•			
GGT	ACT	AAT	GTA	GCC	TCG	TAC	CAG	CAG	AAG	CCA	GGA	AAG	GCT	CCA	AAG	192
G1y	Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
	30					35					40					
CTG	CTC	ATC	TAC	TCC	GCA	TCC	TAT	ccc	TAC	AGT	GGT	GTG	CCA	AGC	AGA	240
					A1a											
45			.,.		50					55					60	
					AGC											288
Phe	Ser	Gly	Ser		Ser	G1y	Thr	Asp		Thr	Phe	Thr	Ile		Ser	
				65					70					75		
CTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TTC	TGC	CAG	CAA	TAT	AAC	AGC	336
															Ser	
			80					85					90			
														_		379
					GGC Gly											3/9
Lyr	FLO	95		Lile	u.y	4711	100	1111	275	141	JIU	105	۵,۰			
SEC	ID			7												
				thi	3	79										
Sec	uen	ce :	Гуре	:	Nuc	leic	ac	id								
	•		ess:		oub.	le										
Top	olo	qy:	Li	nea	E											
Mol	.ecu	lar	Туг	et	Sy	nthe	tic									
Ori	.gin	al :	Sour	ce	.,											
	0	rga	nisn	n :	Моц	5 e 2	ind	hum	an							
Imn	edi	ate	Sou	irce	•											
	С	lone	e:	HEF	-RV	L-M2	1d-	gĸ								
	A	min	o ac	id	-19	1:	lea	der								

Amino acid 1 - 23:FR1

3-114	24 - 34:CDR1											
	. 35 - 49:FR2											
	50 - 56:CDR2											
	57 - 88:FR3											
Amino acid	89 - 97:CDR3											
Amino acid 98 - 107:FR4												
Sequence												
ATG GGA TGG AGC TGT	ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48										
Met Gly Trp Ser Cys	Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly											
-19 -15	-10 -3											
		96										
Val His Ser Asp Ile	Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 5 10											
-1 1	3 10											
AGC GTG GGT GAC AGA	GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	44										
	Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val											
15	20 25											
		92										
Gly Thr Asn Val Ala	Trp Tyr Gin Gin Lys Pro Gly Lys Ala Pro Lys											
30	35 40											
	GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 2	40										
	Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	40										
45	50 55 60											
7.	30 33											
TTC AGC GGT AGC GGT	AGC GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC 2	88										
Phe Ser Gly Ser Gly	Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser											
65	70 75											
		36										
•	Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser											
80	85 90											
TAT COT CGG GCG TTC	GGC CAA GGG ACC AAG GTG GAA ATC AAA C 3	79										
	e Gly Gln Gly Thr Lys Val Glu Ile Lys											
95	100 105											
SEQ ID NO: 48												
Sequence Length:	. 29											

Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
TGACAGAGTG TCCGTCACCT GTAAGGCCA
SEQ ID NO: 49
Sequence Length: 29
Sequence Type: Nucleic acid
Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TTACAGGTGA CGGACACTCT GTCACCCAC

SEQ ID NO: 50

Sequence Length: 379

Sequence Type: Nucleic acid Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human Immediate Source

Clone: HEF-RVL-M21e-gk
Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3
Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

29

29

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48											
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly												
-19 -15 -10 -5												
GTC CAC TCC GAC ATC GAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96											
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala												
-1 5 10												
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	144											
15 20 25												
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192											
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys												
30 35 40												
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240											
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg												
45 50 55 60												
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC AGC ATC AGC AGC Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr IIe Ser Ser	288											
65 70 75												
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336											
Leu Gin Pro Giu Asp Ile Ala Thr Tyr Tyr Cys Gin Gin Tyr Asn Ser												
, 80 85 90												
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379											
Tyr Pro Arg Ala Phe Gly Gin Gly Thr Lys Val Glu Ile Lys												
95 100 105												
SEQ ID NO: 51												
Sequence Length: 379												
Sequence Type: Nucleic acid												
Strandedness: Double												
Topology: Linear												
Molecular Type: Synthetic												
Original Source												
Organism: Mouse and human												
Immediate Source												

										•						
	0	lon	e:	HE	-RV	L-M	21f-	gĸ								
	1	l min	о а	cid	-19	1	:lea	der								
	1	Amin	o a	cid	1	- 1	23:F	RI								
	I	min	o a	cid	24		34 : C	DRI								
	1	Amin	o a	cid	35		49 t F	R2								
	I	min	o a	cid	50	- 3	56:C	DR2								
	I	min	o a	cid	57	- 1	88:F	R3								
	1	lmin	o a	cid	89	- !	97:C	DR3								
	2	min	o ac	cid	98	- :	107:	FR4								
Sec	quer	ice														
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TCC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Ser	Leu	Val	Ala	Thr	Ala	Thr	Gly	
-19				-15					-10					- 5		

							ACC Thr									96
		-1			GIII	rie L	1112	5	Ser	120	261	ser	10		WIR	
			_					-					10			
							GTC									144
Ser	Val		Asp	Arg	Va1	Ser	Va1	Thr	Cys	Lys	Ala		Gln	Asn	Va1	
		15					20					25				
GGT	ACT	AAT	GTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	CCA	AAG	CCT	***	440	192
							Gln									172
	30					35			•		40	•			-,-	
							TAT									240
45	Leu	116	ıyı	241	50 50	ser	Tyr	Arg	Tyr	Ser 55	GIY	Val	Pro	Ser	Arg 60	
															00	
TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	288
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	
				65					70					75		
CTC	CAG	CCA	GAG	GAC	ATC	ccc	ACC	TAC	TTC	TCC	CAC	CAA	74	***	400	22.6
							Thr									336
			80					85		-, -			90	-1011		

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys SEO ID NO: 52 Sequence Length: 26 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 26 GACTTCACCT TGACCATCAG CAGCCT SEO ID NO: 53 Sequence Length: 26 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 26 CTGCTGATGG TCAAGGTGAA GTCGGT SEQ ID NO: 54 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21g-gr Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3	
Amino acid 98 - 107:FR4	
Sequence	
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GGA ACA GCT AGA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGG GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
	24.0
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GTG GTG CCA AGC AGA Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	240
45 SO S5 60	
43 30 33	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gin Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gin Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	
SEQ ID NO: 55	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	

Strandedness: Double Topology: Linear Molecular Type: Synthetic

Ori	gina	al S	our	Ce												
	Oı	cgan	iism	. 1	dous	e a	nd i	numa	ın							
1 mm	edia	ate	Sou	rce												
	Ç.	lone	2 1	HEF-	-RVI	-M2	1h-9	gĸ								
	Ar	ninc	ac	id ·	-19-	-1:	lead	ier								
	AJ	ninc	ac	id	1	- 2	3 : F1	R1								
	Ar	ninc	ac	id	24	- 3	4 : CI	DRI								
	Ar	ninc	ac	id	35	- 4	9 : F1	R2								
	Ar	ninc	3.0	id	50	- 5	6 : CI	DR2								
							8:F									
					-		7 : C1									
_			ac	ıa	98	- 1	07:1	r R4								
	uen															48
									TTG Leu							40
-19	GLY	rrp	ser	-15	116	TTE	Leu	Ser	-10	VAL	AIA	1111	~-4	-5	Cly	
-19				-13					- 40					-		
GTC	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGÇ	ÇTG	AGC	GCC	96
Val	His	Ser	Asp	Ile	Gln	Met	Thr	G1n	Ser	Pro	Ser	Ser	Leu	Ser	A1a	
		-1	1					5					10			
									TGT							144
ser	ANT	15	Asp	Arg	Val	int	20	int	Cys	Lys	VIR	25	GIII	ASII	VAI	
		13					20									
GGT	ACT	AAT	GTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	AAG	GCT	CCA	AAG	192
Gly	Thr	Asn	Va1	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	G1y	Lys	Ala	Pro	Lys	
	30					35					40					
									TAC							240
		Ile	Tyr	5er		Ser	Tyr	Arg	Tyr	Ser 55	GIA	Vai	Pro	ser	Arg 60	
45					50					23					00	
TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTG	ACC	ATC	AGC	AGC	288
									Phe							
				65					70					75		

336 CTC CAG CGA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 379 TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C Tyr Pro Arg Ala Phe Gly Gin Gly Thr Lys Val Glu Ile Lys 100 SEQ ID NO: 56 Sequence Length: 29 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 29 GGACAGAGTC CAAAGCCGCT GATCTACTC SEQ ID NO: 57 Sequence Length: 29 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 29 ATCAGCGGCT TTGGACTCTG TCCTGGCTT SEQ ID NO: 58 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21i-gx Amino acid -19--1:leader Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2	
Amino acid .50 - 56:CDR2	
Amino acid 57 - 88:FR3	
Amino acid 89 - 97:CDR3	
Amino acid 98 - 107:FR4	
Sequence	
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
41 1 3 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Fro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105	
SEQ ID NO: 59	
Sequence Length: 26	
Sequence Type: Nucleic acid	
sednesses this unctate sets	

-19

-15

Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 26 GAGGACATCG CTGACTACTT CTGCCA SEC ID NO: 60 Sequence Length: 26 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 26 AAGTAGTCAG CGATGTCCTC TGGCTG SEQ ID NO: 61 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21j-gx Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4 Sequence ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -10 -5

- / -	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gin Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	1,0
30 35 40	
CCG CTG ATC TAG TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
	200
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTG ACC TTG ACC ATG AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser 65 70 75	
05 /0 13	
CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gin Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gin Gin Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105	
95 100 105 SEQ ID NO: 62	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	
Immediate Source	
Clone: HEF-RVL-M21k-gr	
Amino acid -191-loador	

Clone: HEF-RVL-M21k-gk
Amino acid -19--1:leader
Amino acid 1 - 23:FR1

Amino acid	24 - 34:CDR1		
Amino acid	35 - 49:FR2		
Amino acid	50 - 56:CDR2		
Amino acid	57 - 88:FR3		
Amino acid	89 - 97:CDR3		
Amino acid	98 - 107:FR4		
Sequence			
ATG GGA TGG AGC TGT	ATC ATC CTC TCC	TTG GTA GCA ACA GCT	ACA GGT 48
Met Gly Trp Ser Cys	Ile Ile Leu Ser	Leu Val Ala Thr Ala	Thr Gly
-19 -15		-10	-5
CHC CAC TCC CAC ATC	CAG ATG ACC CAG	AGC CCA AGC AGC CTG	AGC GCC 96
		Ser Pro Ser Ser Leu	
-1 1	:		
		TGT AAG GCC AGT CAG	
		Cys Lys Ala Ser Gln	Asn Val
15	20	25	
GGT ACT AAT GTA GCC	TGG TAC CAG CAG	AAG CCA GGA AAG GCT	CCA AAG 192
		Lys Pro Gly Lys Ala	
30	35	40	
		n man ann com com coca	AGC AGA 240
		G TAC AGT GGT GTG CCA g Tyr Ser Gly Val Pro	
45	50	55	60
		C TTC ACC TTG ACC ATC	
		Phe Thr Leu Thr Ile	
65		70	75
CTC CAG CCA GAG GAG	ATC GCC GAC TA	C TTC TGC CAG CAA TAT	AAC AGC 336
		r Phe Cys Gln Gln Tyr	
80	8	5 90	
		ama ass	c 379
		C AAG GTG GAA ATC AAA r Lys Val Glu Ile Lys	C 3/9
1yr Pro Arg Ala Phe 95	100	105	
SEQ ID NO: 63			
Sequence Length:	: 379		

Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M211-qk Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4 Sequence ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -15 -10 -19 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala -1 1 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144 Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192 Gly Thr Asn Val Als Trp Tyr Gin Gin Lys Pro Gly Gin Ser Pro Lys 35 30 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240 Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 55 45 50

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
	126
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gin Pro Giu Asp fle Ala Thr Tyr Tyr Cys Gin Gin Tyr Asn Ser 80 85 90	
55	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gin Gly Thr Lys Val Glu Ile Lys	
95 100 105	
SEQ ID NO: 64	
Sequence Length: 26	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
CAGAGCCAAA AGTTCCTGAG CGCCAG	26
SEQ ID NO: 65	
Sequence Length: 26	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
CTCAGGAACT TTTGGCTCTG GGTCAT	26
SEQ ID NO: 66	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	
Immediate Source	

- 74 -	
Clone: HEF-RVL-M21m-gx	
Amino acid -191:leader	
Amino acid 1 - 23:FR1	
Amino acid 24 - 34:CDR1	
Amino acid 35 - 49:FR2	
Amino acid 50 - 56:CDR2	
Amino acid 57 - 88:FR3	
Amino acid 89 - 97:CDR3	
Amino acid 98 - 107:FR4	
Sequence	
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CAA AAG TTC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Gln Lys Phe Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
THE STATE OF THE PART THE CASE OF THE COLD AND THE COLD AND	192
GGT AGT AGT GGG TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	192
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 45 50 55 60	
45 50 53	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG GAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	

379 TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 SEC ID NO: 67 Sequence Length: 29 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 29 GGACAGAGTC CAAAGCTGCT GATCTACTC SEO ID NO: 68 Sequence Length: 29 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 29 ATCAGCAGCTT TGGACTCTG TCCTGGCTT SEQ ID NO: 69 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21n-gk Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4	
Sequence	
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	,,,
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
	192
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	192
30 35 40	
30 33	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75	
65 /0 /5	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gin Pro Giu Asp lie Ala Thr Tyr Tyr Cys Gin Gin Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105	
SEQ ID NO: 70	
Sequence Length: 379	
Sequence Type: Nucleic acid	
• ••	
Strandedness: Double	

Topology: Linear Molecular Type: Synthetic

Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M210-gx Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4 Sequence ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48 Met Gly Trp Ser Cys Iie Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -5 -19 -15 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala -1 1 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192 Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 40 30 35 240 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 55 45 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

70

65

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 TAT CCT CGG GCG TTC GGC CAA CGG ACC AAG GTG GAA ATC AAA C 379 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105 SEO ID NO: 71 Sequence Length: 23 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GCTCCAAAGC CGCTGATCTA CTC 23 SEQ ID NO: 72 Sequence Length: 23 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence TAGATCAGCG GCTTTGGAGC CTT 23 SEQ ID NO: 73 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21p-gx Amino acid -19--1:leader Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2	
Amino acid 50 - 56:CDR2	
Amino acid 57 - 88:FR3	
Amino acid 89 - 97:CDR3	
Amino acid 98 - 107:FR4	
Sequence	
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	90
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 45 50 55 60	
45 50 55	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
6 5 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC Leu Gin Pro Glu Asp Ile Alg Thr Tyr Tyr Cys Gin Gin Tyr Asn Ser	336
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	
SEQ ID NO: 74	
Sequence Length: 137	
Sequence Type: Nucleic acid	

Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
AAGAAGCCTG GGTCCTCAGT GAAGGTCTCC TGCAAGGCTT CTGGCTTCAA CATTAAAGAC	60
ACCTATATAC ACTGGGTGCG CCAGGCTCCA GGACAGGGCC TGGAGTGGAT GGGAAGGATT	120
GATCCTGAGG ATGGTAA	137
SEQ ID NO: 75	
Sequence Length: 111	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
TGAGATCTGA GGACACAGCC TTTTATTTCT GTGCAAGTGC CTACTATGTT AACCAGGACT	60
ACTGGGGCCA AGGGACCACT GTCACCGTCT CCTCAGGTGA GTGGATCCGA C	111
SEQ ID NO: 76	
Sequence Length: 130	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACCTTCACTG AGGACCCAGG CTTCTTCACC TCAGCTCCAG ACTGCACCAG CTGCACCTGG	60
GAGTGAGCAC CTGGAGCTAC AGCCAGCAAG AAGAAGACCC TCCAGGTCCA GTCCATGGTC GAAGCTTATC	120 130
SEO ID NO: 77	130
Sequence Length: 132	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
AAAGGCTGTG TCCTCAGATC TCAGGCTGCT GAGCTCCATG TAGGCTGTGT TCGTGGATTC	60
GTCTGCAGTG ATTGTGACTC GGCCCTGGAA CTTCGGGTCA TATTTAGTAT TACCATCCGC	120
AGGATCAATC CT	132

SEQ ID NO: 78 Sequence Length: 25 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GATAAGCTTC CACCATGGAC TGGAC SEO ID NO: 79 Sequence Length: 25 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GTCGGATCCA CTCACCTGAG GAGAC SEQ ID NO: 80 Sequence Length: 409 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVH-M21-gvl Amino acid -19--1:leader Amino acid 1 - 30:FR1 Amino acid 31 - 35:CDR1 Amino acid 36 - 49:FR2 Amino acid 50 - 66:CDR2 Amino acid 67 - 98:FR3

> Amino acid 99 - 106:CDR3 Amino acid 107 - 117:FR4

Sequence

25

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly -19 -15 -5 GCT CAC TCC CAG GTG CAG CTG CAG TCT GGA GCT GAG GTG AAG AAG Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
GCT CAC TCC CAG GTG CAG CTG CTG CAG TCT GGA GCT GAG GTG AAG AAG 96	
-1 1 5 10	
	
CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC TTC AAC ATT	
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile	
15 20 25	
AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA CAG GGC CTG 192	
Lys Asp Thr Tyr Ile His Trp Val Arg Gin Ala Pro Gly Gin Gly Leu	
30 35 40	
GAG TGG ATG GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC 240	
Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp	
45 50 55 60	
CCC ALC TTC OLD CCC CCL CTC ALL CTC ALC CTC	
CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA TCC ACG AAC Pro Lys Phe Gin Giy Arg Val Thr Ile Thr Ala Asp Giu Ser Thr Asn	
65 70 75	
73 /7	
ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACA GCC TTT 336	
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe	
80 85 90	
TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC TGG GGC CAA 384	
Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gin Asp Tyr Trp Gly Gin 95 100 105	
95 100 105	
GGG ACC ACT GTC ACC GTC TCC TCA G	
Gly Thr Thr Val Thr Val Ser Ser	
110 115	
SEQ ID NO: 81	
Sequence Length: 84	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	

Molecular Type: Synthetic DNA	
Sequence	
AGCTTGTCAC CGTCTCCTCA GGTGCTCGTG GTTCGGGTGG TGGTGGTTCG GGTGGTGGCG	60
GATCGGACAT CCAGATGACC CAGG	84
SEQ ID NO: 82	
Sequence Length: 84	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
AATTCCTGGG CCATCTGGAT GTCCGATCCG CCACCACCG AACCACCACC ACCCGAACCA	60
CCACCACCTG AGGAGACGGT GACA	84
SEQ ID NO: 83	
Sequence Length: 34	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG	34
SEQ ID NO: 84	
Sequence Length: 41	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
CCACCCGAAC CACCACCA TGAGGAGACG GTGACAGTGG T	41
SEQ ID NO: 85	
Sequence Length: 41	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	

Sequence	
GGGACCACTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G	41
SEQ ID NO: 86	
Sequence Length: 41	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A	41
SEQ ID NO: 87	
Sequence Length: 44	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
TCGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG	44
SEQ ID NO: 88	
Sequence Length: 57	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
CAAGAATTCT TATTATTTAT CGTCATCGTC TTTGTAGTCT TTGATTTCGA CCTTGGT	57
SEQ ID NO: 89	
Sequence Length: 822	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	
Immediate Source	

	Ç:	lone	:	pSC	evr7	-hM	21									•	
	A	ninc	ac	id	.1 -	- 22	:lea	adei	:								
	Aı	ninc	ac	id	23	-	139	:н с	hai	n V	reg	ion					
Amino acid 140 - 154:Linker																	
Amino acid 155 - 261:L chain V region																	
	Aı	ninc	ac	id	262	-	269	FLA	\G								
	Aı	ninc	ac	id :	segu	enc	e o	E Fr	г ро	lyp	epti	de	scF	v-hl	121	and	
	nucleotide sequence coding therefor																
Sequence																	
											TTG						48
Met	Lys	Tyr	Leu		Pro	Thr	Ala	Ala		Gly	Leu	Leu	Leu		Ala		
				5					10					15			
GCC	CAA	CCA	GCC	ATG	GCG	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGA	GCT	GAG		96
Ala	GIn	Pro	Ala	Met	Ala	Gln	Val	Gln	Leu	Val	G1n	Ser	Gly	Ala	Glu		
			20					25					30				
c e c					mcc.	mc 4	cac		CTC	TCC	TGC	440	CCT	TOT			144
											Cys						144
	-,-	35		,			40	_, -			-,-	45			•		
											CGC						192
Phe	Asn 50	Ile	Lys	Asp	Thr	Tyr 55	Ile	His	Trp	Val	Arg 60	GIn	Ala	Pro	GLY		
	30					33					00						
CAG	GGC	CTG	GAG	TGG	ATG	GGA	AGG	ATT	GAT	CCT	GCG	GAT	GGT	AAT	ACT		240
	Gly	Leu	Glu	Trp		Gly	Arg	Ile	Asp		Ala	Asp	Gly	Asn			
65					70					75					80		
AAA	TAT	GAC	CCG	AAG	TTC	CAG	GGC	CGA	GTC	ACA	ATC	ACT	GCA	GAC	GAA		288
											Ile						
				85					90					95			
											CTG Leu						336
201			100		.,.		JIU	105	261	-01			110				

TAATAAGAAT TOTTG

ACA	GCC	TTT	TAT	TTC	TGT	GCA	AGT	ccc	TAC	TAT	GTT	AAC	CAG	GAC	TAC	38	4
Thr	Ala	Phe	Tyr	Phe	Cys	Ala	Ser	Ala	Tyr	Tyr	Va1	Asn	Gln	Asp	Tyr		
		115					120					125					
TGG																43	2
Trp	G1y	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser		
	130					135					140						
		_										~.~	4.00	400	CAG	48	n
GGT																***	•
Gly	Gly	Gly	GIY	Ser		GIA	GIĀ	GIÀ			TIA	GIII	Mec	1111	160		
145					150					155					100		
AGC	CCA	AGC	AGC	CTG	AGC	GCC	AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	52	8
				Leu													
				165					170					175			
				CAG												57	6
Cys	Lys	Ala	Ser	Gln	Asn	Val	Gly	Thr	Asn	Va1	Ala	Trp	Tyr	Gln	Gln		
			180					185					190				
															CGG	62	4
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro	Leu	lle	Tyr	Ser			Tyr	Arg		
		195					200					205					
				CCA							cen	400	cer	Acc	CAC	61	,,
															Asp	•	-
Tyr			AST	Pro	ser			261	GLY	ser	220		G1 ,	****	nap		
	210					215					220						
TTC	ACC	TTC	ACC	ATC	AGC	AGC	CTC	CAG	CCA	GAG	GAC	ATC	GCT	ACC	TAC	7	20
															Tyr		
225					230					235					240		
															ACC	7	68
Tyr	Сув	Gln	Gln	Tyr	Asn	Ser	Tyr	Pro	Arg	Ala	Phe	Gly	Glr	Gly	Thr		
				243					250					255	i		
																•	07
				AAA												8	.,
Lys	Val	Glu		Lys	ASP	Tyx	- PAs			waf	, wel	, Lys	•				
			260	,				265	1								
TAA	TAAG	TAA	TCTT	'G												8	22

SEQ ID NO: 90

Sequence Length: 45

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Features: Amino acid sequence of linker region of Fv polypeptide

and nucleotide sequence coding therefor

Sequence

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

15